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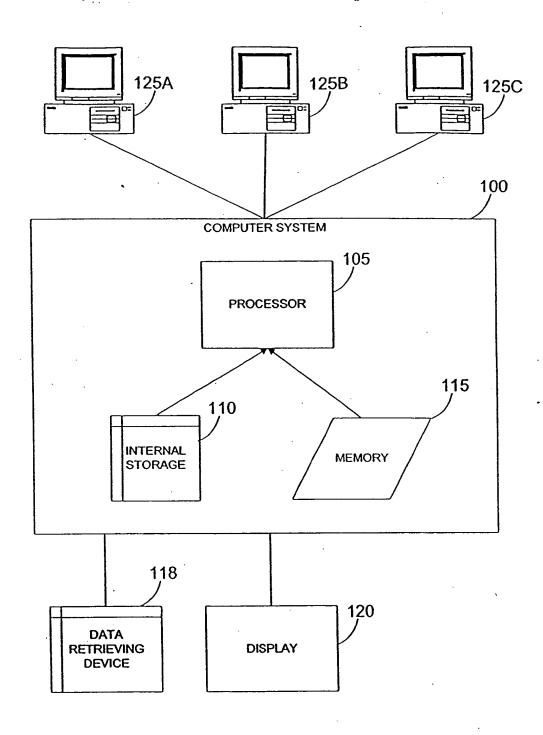


FIGURE !

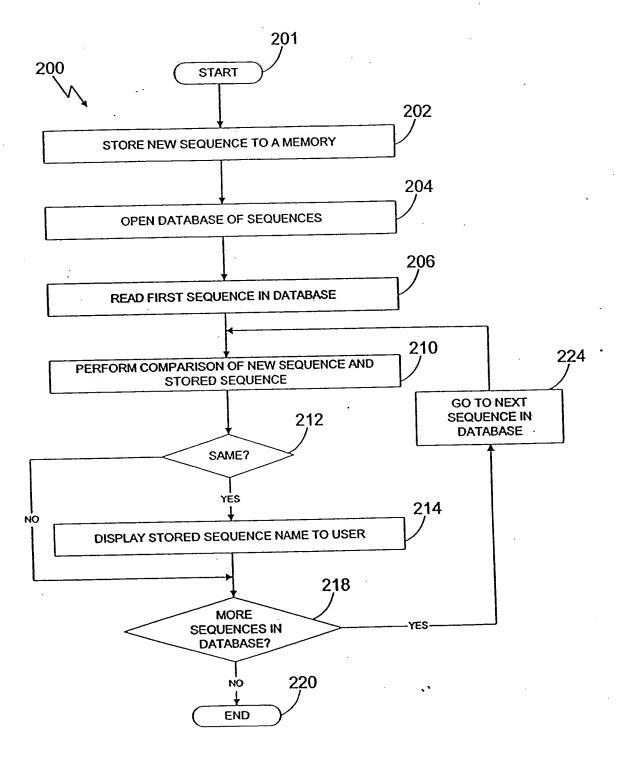
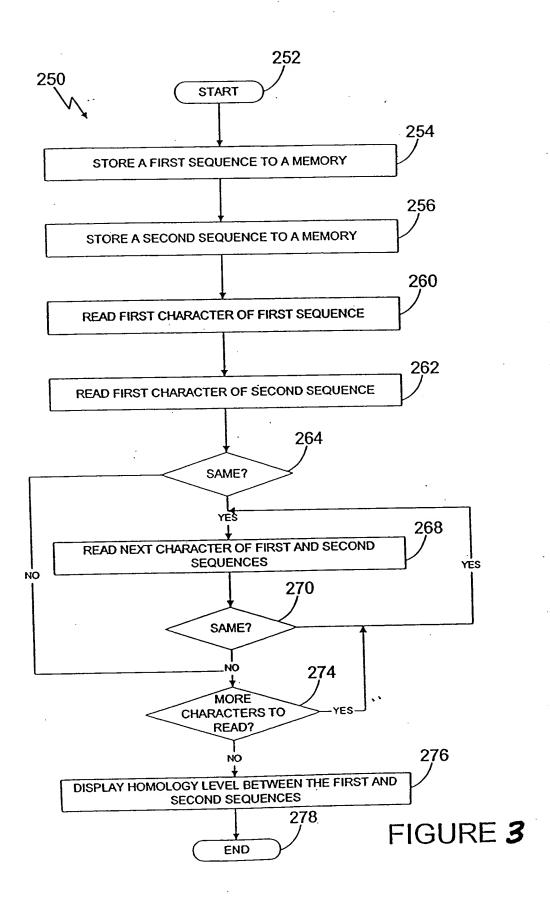


FIGURE 2



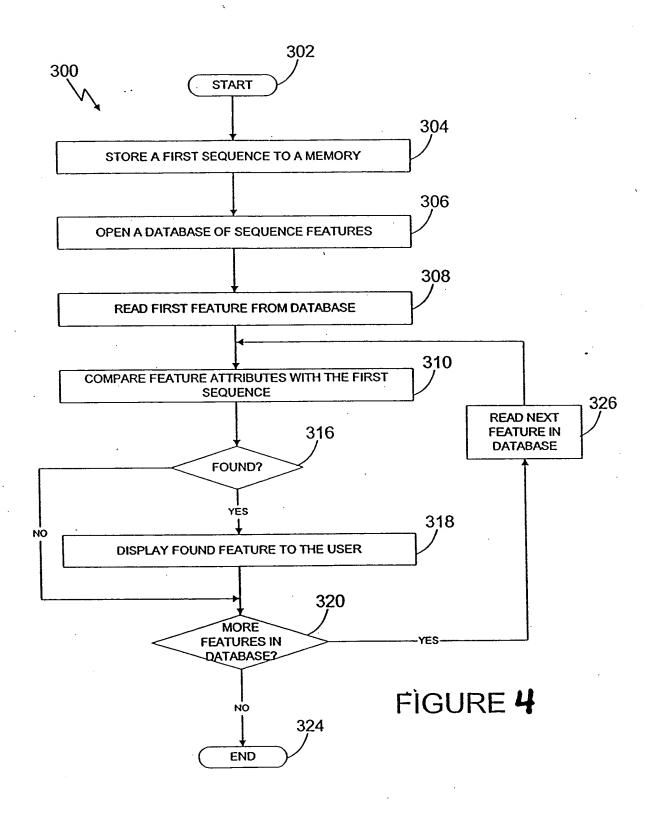


FIGURE 5

Ammonifex degensii KC4 Phosphatase(3A1A=3A2A) Complete gene sequence

	ATGAGGGGGAGCGGAGTGCGGATACTTCTCACCAACGATGACGGCATCTTTGCCGAGGGT
1	MetArgGlySerGlyValArgIleLeuLeuThrAsnAspAspGlyIlePheAlaGluGly
	CTGGGGGCTCTGCGCAAGATGCTGGAGCCCGTGGCTACCCTTTACGTGGTGGCTCCGGAC
21	LeuGlyAlaLeuArgLysMetLeuGluProValAlaThrLeuTyrValValAlaProAsp
	CGAGAGCGTAGCGCCAGCCATGCTATCACCGTTCACCGCCCCCTGCGGGTGCGGGAG
41	ArgGluArgSerAlaAlaSerHisAlaIleThrValHisArgProLeuArgValArgGlu
	GCGGGTTTTCGCAGCCCAGGCTTAAAGGCTGGGTAGTGGACGGTACCCCGGCCGACTGC
61	AlaGlyPheArgSerProArgLeuLysGlyTrpValValAspGlyThrProAlaAspCys
	GTCAAGCTGGGCCTGGAGGTACTTTTGCCCGAACGTCCAGATTTCCTGGTTTCGGGCATA
81	ValLysLeuGlyLeuGluValLeuLeuProGluArgProAspPheLeuValSerGlyIle
	AACTACGGGCCCAACCTGGGTACCGACGTACTTTACTCCGGCACCGTCTCGGCGGCCATA
101	AsnTyrGlyProAsnLeuGlyThrAspValLeuTyrSerGlyThrValSerAlaAlaIle
	GAAGGGGTAATTAACGGCATTCCCTCGGTGGCCGTATCTTTGGCCACGCGGGGAGCCG
121	GluGlyValIleAsnGlyIleProSerValAlaValSerLeuAlaThrArgArgGluPro
	GACTATACCTGGGCGGCCCGGTTCGTCCTGGTCCTGGAGGAACTGCGAAAACACCAA
141	AspTyrThrTrpAlaAlaArgPheValLeuValLeuLeuGluGluLeuArgLysHisGln
	CTGCCCCAGGAACCCTGCTCAACGTCACGTGCCCGACGGGGTGCCCCGCGGGGTCAAG
161	LeuProProGlyThrLeuLeuAsnValAsnValProAspGlyValProArgGlyValLys
	GTGACCAAACTGGGAAGCGTACGCTACGTCAACGTGGTAGACTGCCGCACCGACCCTCGG
181	ValThrLysLeuGlySerValArgTyrValAsnValValAspCysArgThrAspProArg
	GGGAAGGCTTACTACTGGATGGCGGGAGAACCATTGGAGCTGGACGGCAACGACTCCGAA
201	GlyLysAlaTyrTyrTrpMetAlaGlyGluProLeuGluLeuAspGlyAsnAspSerGlu
	ACCGACGTCTGGGCGGTGCGAGAAGGCTATATTTCCGTAACACCGGTCCAGATCGACCTT
221	ThrAspValTrpAlaValArgGluGlyTyrIleSerValThrProValGlnIleAspLeu
	ACTAACTACGGCTTCCTGGAAGAACTCAAAAAATGGCGTTTCAAGGATATCTTTTCTTCT
241	Thr Asn Tyr Gly Phe Leu Glu Glu Leu Lys Lys Trp Arg Phe Lys Asp Ile Phe Ser Ser Lys Asp Ile Phe Ser Lys Asp Ile Phe Ser Lys Asp Ile Phe Ser Ser Lys Asp Ile Phe Ser Lys Asp Ile Phe Ser Lys Asp Ile Phe Ser Ser Lys Asp Ile Phe Ser
	TAA
261	End 261

1/

FIGURE 6

Methanococcus igneus Kol5 Phosphatase (9AlA) Complete Gene Sequence

	ATGTTGGATATACTGCTTGTTAATGATGATGGCATTTATTCAAATGGATTAATAGCTTTG
1	MetLeuAspIleLeuLeuValAsnAspAspGlyIleTyrSerAsnGlyLeuIleAlaLeu
	AAGGATGCATTATTGGAAAAATTTAATGCGAGGATTACTATTGTAGCCCCAACAAATCAG
21	LysAspAlaLeuLeuGluLysPheAsnAlaArgIleThrIleValAlaProThrAsnGln
	CAGAGTGGTATTGGTAGGGCAATAAGTTTATTCGAGCCGTTAAGGATAACTAAAACCAAA
41	GlnSerGlyIleGlyArgAlaIleSerLeuPheGluProLeuArgIleThrLysThrLys
	TTAGCAGATGGTTCTTGGGGATATGCAGTTTCAGGAACCCCAACAGATTGCGTTATATTG
61	LeuAlaAspGlySerTrpGlyTyrAlaValSerGlyThrProThrAspCysValIleLeu
	GGCATTTATGAGATATTAAAGAAGGTACCTGATGTAGTTATATCAGGAATAAACATTGGA
81	GlyIleTyrGluIleLeuLysLysValProAspValValIleSerGlyIleAsnIleGly
	GAAAACCTTGGGACTGAAATAACAACTTCTGGAACGTTGGGGGCTGCGTTTGAAGGGGCC
101	GluAsnLeuGlyThrGluIleThrThrSerGlyThrLeuGlyAlaAlaPheGluGlyAla
	CATCATGGGGCTAAGGCATTAGCATCATCACTCCAAGTTACCTCTGACCATCTAAAGTTT
121	HisHisGlyAlaLysAlaLeuAlaSerSerLeuGlnValThrSerAspHisLeuLysPhe
	AAAGAGGGGGAGACCCCAATAGACTTCACAGTCCCAGCAAGAATTACTGCAAATGTTGTT
141	LysGluGlyGluThrProIleAspPheThrValProAlaArgIleThrAlaAsnValVal
	GAGAAGATGTTGGATTATGATTTCCCATGTGATGTCGTCAACTTAAACATTCCAGAAGGA
161	GluLysMetLeuAspTyrAspPheProCysAspValValAsnLeuAsnIleProGluGly
	GCAACAGAAAAGACACCGATTGAAATCACAAGGTTGGCAAGGAAAATGTATACAACACAC
181	AlaThrGluLysThrProIleGluIleThrArgLeuAlaArgLysMetTyrThrThrHis
	GTTGAGGAAAGAATAGATCCAAGAGGGAGGAGTTATTATTGGATTGATGGGTATCCTATT
201	ValGluGluArgIleAspProArgGlyArgSerTyrTyrTrpIleAspGlyTyrProIle
	TTAGAGGAAGAGACACTGATGTCTATGTTGTTAGAAGAAAGGGACATATTTCTCTA
221	LeuGluGluGluAspThrAspValTyrValValArgArgLysGlyHisIleSerLeu
	ACCCCATTAACATTAGACACAACAATTAAAAATTTAGAGGAATTTAAGAAAAAAATATGAG
241	ThrProLeuThrLeuAspThrThrIleLysAsnLeuGluGluPheLysLysLysTyrGlu
	AGAATATTAAATGAATGA
261	ArgIleLeuAsnGluEnd 266

FIGURE 7

Thermococcus alcaliphilus AEDII12RA Phosphatase (18A) Complete Gene Sequence

	ATGATGATGGAATTCACTCGCGAGGGAATAAAAGCTGCTGTAGAGGCACTTCAAGGGTTA
1	
	GGAGAGATCTACGTAGTTGCCCCAATGTTTCAAAGGAGCGCAAGTGGAAGGGCAATGACC
21	GlyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr
	ATCCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCAAAAGCAGCCTATGCT
41	IleHisArgProLeuArgAlaLysArgIleSerMetAsnGlyAlaLysAlaAlaTyrAla
	TTGGATGGAATGCCCGTTGATTGCGTTATCTTTGCCATGGCCAGATTTGGAGATTTCGAC
61	LeuAspGlyMetProValAspCysValIlePheAlaMetAlaArgPheGlyAspPheAsp
	CTTGCAATAAGTGGTGTAAACTTGGGAGAAAACATGAGCACCGAGATAACGGTTTCCGGG
81	LeuAlaIleSerGlyValAsnLeuGlyGluAsnMetSerThrGluIleThrValSerGly
	ACTGCAAGCGCTGCAATAGAGGCTGCAACCCAAGAGATCCCAAGCATTCCCATAAGCCTG
101	ThrAlaSerAlaAlaIleGluAlaAlaThrGlnGluIleProSerIleProIleSerLeu
	GAAGTTAATAGAGAAAAACACAAATTTGGTGAGGGCGAAGAGATTGACTTCTCAGCTGCC
121	GluValAsnArgGluLysHisLysPheGlyGluGlyGluGluIleAspPheSerAlaAla
	AAGTATTTCCTAAGAAAAATCGCAACGGCGGTTTTAAAGAGAGGCCTCCCCAAAGGAGTC
141	LysTyrPheLeuArgLysIleAlaThrAlaValLeuLysArgGlyLeuProLysGlyVal
	GATATGCTGAACGTCAACGTCCCTTATGATGCAAATGAAAGGACAGAGATAGCTTTTACT
161	AspMetLeuAsnValAsnValProTyrAspAlaAsnGluArgThrGluIleAlaPheThr
	CGCCTGGCAAGAAGGATGTATAGGCCTTCTATTGAAGAGCGCATAGACCCAAAGGGGAAT
181	ArgLeuAlaArgArgMetTyrArgProSerIleGluGluArgIleAspProLysGlyAsn
	${\tt CCCTACTACTGGATAGTTGGAACTCAGTGCCCTAAGGAGGCATTAGAGCCGGGAACGGAT}$
201	ProTyrTyrTrpIleValGlyThrGlnCysProLysGluAlaLeuGluProGlyThrAsp
	ATGTATGTAGTTAAAGTTGAGAGAAAAGTTAGCGTGACTCCAATAAACATTGATATGACA
221	MetTyrValValLysValGluArgLysValSerValThrProIleAsnIleAspMetThr
	GCAAGAGTGAATTTAGACGAGATTAAAAGACTTTTAGAACTGTAG
241	AlaArgValAsnLeuAspGluIleLysArgLeuLeuGluLeuEnd 255

FIGURE 8

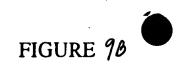
Thermococcus celer Phosphatase (25A1A) Complete Gene Sequence

	ATGAGAACCCTGACAATAAACACTGACGCGGAGGGGTTCGTTTTGAGGATTCTCCTGACG	
1		20
	AACGACGATGGAATCTACTCCAACGGACTGCGCGCCGCTGTGAAAGCCCTGAGTGAG	
21	AsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaValLysAlaLeuSerGluLeu	40
	GGCGAAGTTTACGTCGTTGCCCCCCTCTTCCAGAGGAGCGCGAGCGGCAGGGCCATGACG	
41	GlyGluValTyrValValAlaProLeuPheGlnArgSerAlaSerGlyArgAlaMetThr	60
	CTCCACAGGCCGATAAGGGCCAAGCGĆGTTGACGTTCCCGGCGCAAAGATAGCCTACGGA	
61	LeuHisArgProIleArgAlaLysArgValAspValProGlyAlaLysIleAlaTyrGly	80
	ATAGATGGAACTCCTACTGACTGCGTGATTTTCGCCATAGCCCGCTTCGGGAGCTTTGGT	
81	IleAspGlyThrProThrAspCysValllePheAlaIleAlaArgPheGlySerPheGly	100
	TTAGCCGTGAGCGGGATTAACCTCGGCGAGAACCTGAGCACCGAGATAACAGTCTCAGGG	
101	LeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThrGluIleThrValSerGly	120
	ACGCCTCCGCTGCCATAGAGGCCTCAACTCATGGAATTCCGAGCATAGCGATTAGCCTT	
121	ThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIleProSerIleAlaIleSerLeu	140
	GAGGTGGAGTGGAAGAAGACCCTCGGCGAGGGTGAGGGGGGTTGACTTCTCGGTCTCGACT	
141	GluValGluTrpLysLysThrLeuGlyGluGlyGluGlyValAspPheSerValSerThr	160
	CACTTCCTCAAGAGAATCGCGGGAGCCCTCTTGGAGAGAGGTCTTCCTGAGGGCGTTGAC	
161	HisPheLeuLysArgIleAlaGlyAlaLeuLeuGluArgGlyLeuProGluGlyValAsp	180
	ATGCTCAACGTCAACGTTCCGAGCGACGCGACGGAGGAAACGGAGATAGCAATCACCCGC	
181	MetLeuAsnValAsnValProSerAspAlaThrGluGluThrGluIleAlaIleThrArg	200
	TTAGCCCGGAAGCGCTACTCCCCAACGGTCGAGGAGAGGATTGACCCCAAGGGCAACCCC	
201	LeuAlaArgLysArgTyrSerProThrValGluGluArgIleAspProLysGlyAsnPro	220
	TACTACTGGATTGTCGGCAAACTTGTCCAAGACTTCGAGCCAGGGACAGATGCCTACGCC	
221	TyrTyrTrpIleValGlyLysLeuValGlnAspPheGluProGlyThrAspAlaTyrAla	240
	CTGAAGGTCGAGAGGAAGGTCAGCGTCACGCCGATAAACATAGATATGACTGCGAGGGTG	
241	LeuLysValGluArgLysValSerValThrProIleAsnIleAspMetThrAlaArgVal	260
	GACTTTGAGGAGCTTGTAAGGGTTCTGTGGGTGTAA	
261	AspPheGluGluLeuValArgValLeuTrpValEnd 272	



Thermococcus GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 1 of 2)

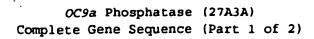
	ATGAAAGGAAAGTCTCTTGTTAGCGGTCTGTTGTTGGGTCTTTTAATTTTGAGCCTGATT	
1	MetLysGlyLysSerLeuValSerGlyLeuLeuLeuGlyLeuLeuIleLeuSerLeuIle	20
	TCATTCCAGCCAAGCTTTGCATACTCCCCACACGGCGGTGTCAAAAACATCATAATCCTG	
21	$Ser Phe Gln Pro Ser Phe Ala Tyr Ser Pro His Gly Gly Val Lys {\tt AsnIleIleIleLeu}$	40
	GTTGGAGACGCCATGGGTCTTGGGCATGTAGAAATTACAAAGCTCGTTTATGGACACTTA	
41	ValGlyAspGlyMetGlyLeuGlyHisValGluIleThrLysLeuValTyrGlyHisLeu	60
	AACATGGAAAACTTTCCAGTTACTGGATTTGAGCTTACTGATTCCCTAAGTGGTGAAGTT	
61	AsnMetGluAsnPheProValThrGlyPheGluLeuThrAspSerLeuSerGlyGluVal	80
	ACAGATTCTGCTGCGGCAGGAACTGCAATATCCACTGGAGCTAAAACGTATAATGGTATG	100
81	ThrAspSerAlaAlaAlaGlyThrAlaIleSerThrGlyAlaLysThrTyrAsnGlyMet	100
	ATTTCAGTAACCAACATAACCGGAAAGATAGTTAACTTAACAACCCTACTTGAAGTGGCT	101
101	IleSerValThrAsnIleThrGlyLysIleValAsnLeuThrThrLeuLeuGluValAla	120
	CAAGAGCTTGGGAAGTCAACAGGGCTGGTCACCACAACAAGGATTACCCATGCAACTCCA	2.47
121	GlnGluLeuGlyLysSerThrGlyLeuValThrThrThrArgIleThrHisAlaThrPro	140
	GCAGTTTTTGCGTCCCATGTCCCAGATAGGGATATGGAGGGGGGAGATACCCAAGCAACTC	
141	AlaValPheAlaSerHisValProAspArgAspMetGluGlyGluIleProLysGlnLeu	160
	ATAATGCACAAAGTTAACGTCTTGTTGGGTGGTGGAAGGGAAAATTCGATGAGAAAAAT	100
161	lleMetHisLysValAsnValLeuLeuGlyGlyGlyArgGluLysPheAspGluLysAsn	180
	TTGGAGCTGGCCAAAAAGCAGGGATACAAAGTAGTTTTCACGAAGGAAG	200
181	LeuGluLeuAlaLysLysGlnGlyTyrLysValValPheThrLysGluGluLeuGluLys	200
	GTTGAAGGAGATTATGTCCTAGGACTCTTTGCAGAAAGTCACATCCCTTACGTATTGGAT	
201	ValGluGlyAspTyrValLeuGlyLeuPheAlaGluSerHisIleProTyrValLeuAsp	220
	AGAAAACCCGATGATGTTGGACTTTTAGAAATGGCCAAAAAGGCAATTTCAATACTCGAG	240
221	ArgLysProAspAspValGlyLeuLeuGluMetAlaLysLysAlaIleSerIleLeuGlu	240
	AAGAACCCGAGCGGATTCTTTCTCATGGTTGAGGGCGGAAGGATTGACCATGCAGCCCAT	260
241	LysAsnProSerGlyPhePheLeuMetValGluGlyGlyArgIleAspHisAlaAlaHis	260
	GGAAACGATGTCGCATCGTTGTTGCAGAAACTAAGGAGTTTGACGATGTTGTCAGATAC	200
261	GlyAsnAspValAlaSerValValAlaGluThrLysGluPheAspAspValValArgTyr	280
	GTGCTGGAATATCCGAAGAAGAGGGGAGATACCTTGGTAATAGTGCTTGCCGATCACGAA	200
281	ValLeuGluTyrProLysLysArgGlyAspThrLeuValIleValLeuAlaAspHisGlu	300
	ACTGGAGGTCTTGCAATAGGTCTAACGTATGGAAATGCAATCGATGAAGATGCCATAAGA	320
301	ThrGlyGlyLeuAlaIleGlyLeuThrTyrGlyAsnAlaIleAspGluAspAlaIleArg	320
	AAAATAAAAGCAAGCACCTTTGAGGATGCCCAAAGAGGTTAAGGCAGGGAGTAGTGTAAAA	240
221	Lugilatugala Sorth, LeuaruMet ProlivsGluVallivsAlaGlvSerSerVallivs	340



Thermococcus GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 2 of 2)

	GAGTCCTCAAAGGTATGCCGGATTTGTCCCAACAGAGGAAGAAGTCAGTATATTGAGAAT	
341	GluSerSerLysValCysArgIleCysProAsnArgGlyArgSerGlnTyrIleGluAsn	360
	GCGCTGCACTCGACAAACAAGTATGCCCTCTCAAATGCAGTAGCCGATGTTATAAACAGG	
361	AlaLeuHisSerThrAsnLysTyrAlaLeuSerAsnAlaValAlaAspValIleAsnArg	380
	CGTATTGGTGTTGGATTCACCTCCTATGAGCATACAGGAGTTCCAGTTCCGCTCTTAGCT	
381	${\tt ArgIleGlyValGlyPheThrSerTyrGluHisThrGlyValProValProLeuLeuAla}$	400
	TACGGTCCCGGGCAGAGAACTTCAGAGGTTTCTTACACCATGTGGATACAGCAAGATTA	
401	TyrGlyProGlyAlaGluAsnPheArgGlyPheLeuHisHisValAspThrAlaArgLeu	420
	GTTGCAAAGTTAATGCTCTTTGGAAGGAGGAATATTCCAGTTACCATTTCAAGCGTGAGC	
421	ValAlaLysLeuMetLeuPheGlyArgArgAsnIleProValThrIleSerSerValSer	440
	AGTGTTAAGGGAGACATAACCGGTGATTACAGGGTTGATGAGAAGGATGCCTACGTTACG	
441	SerValLysGlyAspIleThrGlyAspTyrArgValAspGluLysAspAlaTyrValThr	460
	CTCATGATGTTTCTCGGAGAAAAGTGGATAATGAAATTGAAAAGAGAGTCGATATAGAC	
461	LeuMetMetPheLeuGlyGluLysValAspAsnGluIleGluLysArgValAspIleAsp	480
	AACAACGGCATGGTTGACTTAAATGACGTCATGTTGATTCTCCAGGAAGCTTGA	
481	AsnAsnGlyMetValAspLeuAsnAspValMetLeuIleLeuGlnGluAlaEnd 498	

FIGURE 10A



	ATGCCAAGAAATATCGCCGCTGTATGCGCCCTGGCCGCTTTGTTAGGGTCGGCCTGGGCG	
1	MetProArgAsnIleAlaAlaValCysAlaLeuAlaAlaLeuLeuGlySerAlaTrpAla	20
	GCCAAAGTTGCCGTCTACCCCTACGACGGAGCCGCTTTGCTGGCGGGGCAGCGCTTCGAT	
21	AlaLysValAlaValTyrProTyrAspGlyAlaAlaLeuLeuAlaGlyGlnArgPheAsp	40
	TTGCGCATAGAAGCCTCCGAGCTGAAAGGCAATTTAAAGGCTTACCGCATCACCCTGGAC	
41	LeuArgIleGluAlaSerGluLeuLysGlyAsnLeuLysAlaTyrArgIleThrLeuAsp	60
	GGCCAGCCTCTGGCGGGCCTCGAGCAAACCGCGCAGGGGGGCGGGC	
61	GlyGlnProLeuAlaGlyLeuGluGlnThrAlaGlnGlyAlaGlyGlnAlaGluTrpThr	80
	CTGCGCGGTGCCTTCCTGCGCCCTGGAAGCCACACCCTCGAGGTCAGCCTCACCGACGAC	
81	LeuArgGlyAlaPheLeuArgProGlySerHisThrLeuGluValSerLeuThrAspAsp	100
	GCTGGGGAGAGAGAGAGCGTACGTTGGGAGGCTCGGCAGAACCTTCGCTTGCCCCGA	
101	AlaGlyGluSerArgLysSerValArgTrpGluAlaArgGlnAsnLeuArgLeuProArg	120
	GCGGCCAAGAATGTGATTCTCTTCATTGGCGACGGGATGGGCTGGAACACCCTCAACGCC	
121	AlaAlaLysAsnValIleLeuPheIleGlyAspGlyMetGlyTrpAsnThrLeuAsnAla	140
	GCCCGCATCATCGCCAAAGGCTTTAACCCCGAAAACGGTATGCCCAACGGAAACCTCGAG	
141	AlaArgIleIleAlaLysGlyPheAsnProGluAsnGlyMetProAsnGlyAsnLeuGlu	160
161	ATCGAGAGTGGTTACGGTGGGATGGCTACCGTCACTACCGGCAGCTTTGATAGCTTCATC	100
101	IleGluSerGlyTyrGlyGlyMetAlaThrValThrThrGlySerPheAspSerPheIle	180
101	GCCGACTCAGCTAACTCGGCTTCTTCCATCATGACCGGGCAGAAGGTGCAGGTGAATGCC	200
181	AlaAspSerAlaAsnSerAlaSerSerIleMetThrGlyGlnLysValGlnValAsnAla	200
201	CTCAACGTTTACCCATCAAACCTCAAAGATACCCTGGCCTACCCCCGGATCGAAACCCTA	220
201	LeuAsnValTyrProSerAsnLeuLysAspThrLeuAlaTyrProArgIleGluThrLeu	220
221	GCGGAGATGCTCAAGCGGGTACGCGGGGCCAGCATTGGGGTAGTGACCACCACCTTCGGC AlaGluMetLeuLysArgValArgGlyAlaSerIleGlyValValThrThrThrPheGly	240
221	And twice the unity of the transfer of the tra	240
241	ACCGACGCTACCCCGGCTTCACTCAACGCCCATACCCGCCGCCGCGGTGATTACCAGGCT ThrAspAlaThrProAlaSerLeuAsnAlaHisThrArgArgArgGlyAspTyrGlnAla	260
261	ATCGCCGACATGTACTTTGGTAGAGGCGGGTTCGGTGTTCCCTTGGATGTGATGCTCTTC IleAlaAspMetTyrPheGlyArgGlyGlyPheGlyValProLeuAspValMetLeuPhe	280
281	GGTGGTTCACGCGACTTCATCCCCCAGAGCACCCCTGGCTCGCGCGCAAGGATAGCACG GlyGlySerArgAspPheIleProGlnSerThrProGlySerArgArgLysAspSerThr	300
301	GACTGGATTGCCGAATCCCAGAAGCTGGGCTACACCTTTGTCAGCACCCGCAGCGAGCTG AspTrpIleAlaGluSerGlnLysLeuGlyTyrThrPheValSerThrArgSerGluLeu	320
321	CTGGCGGCCAAACCCACCGATAAGCTGTTTTGGGCTGTTCAACATTGACAACTTCCCCAGC LeuAlaAlaLysProThrAspLysLeuPheGlyLeuPheAsplleAspAspPheProSer	340

FIGURE 10B

OC9a Phosphatase (27A3A) Complete Gene Sequence (Part 2 of 2)

	TACCTAGACCGCGCAGTGTGGAAGCGGCCCGAGATGCTGGGAAGCTTTACCGATATGCCC	
341	TyrLeuAspArgAlaValTrpLysArgProGluMetLeuGlySerPheThrAspMetPro	360
	TACCTCTGGGAGATGACCCAGAAAGCCGTGGAGGCTCTCTCCAGAAACGACAAAGGCTTT	
361	TyrLeuTrpGluMetThrGlnLysAlaValGluAlaLeuSerArgAsnAspLysGlyPhe	380
	TTCTTGATGGTTGAGGGGGGAATGGTGGATAAGTACGAGCACCCCTTGGACTGGCCCCGC	
381	PheLeuMetValGluGlyGlyMetValAspLysTyrGluHisProLeuAspTrpProArg	400
	GCACTTTGGGATGTACTCGAGCTGGACCGCGCGGTGGCTTGGGCCAAGGGCTATGCGGCC	
401	AlaLeuTrpAspValLeuGluLeuAspArgAlaValAlaTrpAlaLysGlyTyrAlaAla	420
	TCCCACCCGATACCCTGGTGATTGTCACCGCCGACCACGCTCACTCGATCTCGGTGTTT	
421	SerHisProAspThrLeuValIleValThrAlaAspHisAlaHisSerIleSerValPhe	440
	GGCGGTTACGACTACTCCAAGCAGGGCCGGGGGGGGGGG	
441	GlyGlyTyrAspTyrSerLysGlnGlyArgGluGlyValGlyValTyrGluAlaAlaLys	460
	TTCCCCACCTACGGCGACAAAAAAGACGCCAACGGCTTTCCCTTGCCCGACACCACTCGG	
461	PheProThrTyrGlyAspLysLysAspAlaAsnGlyPheProLeuProAspThrThrArg	480
	GGAATCGCGGTAGGCTTCGGGGCCACGCCGGATTACTGTGAAACCTACCGGGGCCGCGAG	
481	GlyIleAlaValGlyPheGlyAlaThrProAspTyrCysGluThrTyrArgGlyArgGlu	500
	GTCTACAAAGACCCCACCATCTCCGACGGCAAAGGTGGTTACGTGGCCAACCCTGAGGTC	
501	ValTyrLysAspProThrIleSerAspGlyLysGlyGlyTyrValAlaAsnProGluVal	520
	TGCAAGGAGCCGGGCCTTCCAACGTACCGGCAACTCCCAGTAGATAGCGCCCAGGGCGTG	
521	CysLysGluProGlyLeuProThrTyrArgGlnLeuProValAspSerAlaGlnGlyVal	540
	CACACGGCTGATCCCATGCCGCTGTTTGCCTTTGGCGTGGGGTCTCAGTTCTTCAATGGC	
541	HisThrAlaAspProMetProLeuPheAlaPheGlyValGlySerGlnPhePheAsnGly	560
	CTCATCGACCAGACCGAGATCTTCTTCCGCATGGCCCAGGCCCTAGGGTTCAACCCCCAC	r.o.c
61	LeuIleAspGlnThrGluIlePhePheArgMetAlaGlnAlaLeuGlyPheAsnProHis	580
	CTCGAGAAGCCTTAA	
	range interpretation 585	

FIGURE //

Mll TL Phosphatase (29A1A=29A2A) Complete Gene S quence

	ATGTATAAATGGATTATTGAGGGTAAGCTTGCCCAAGCACCTTTTCCAAGCCTAGGTGAA	
1	MetTyrLysTrpIleIleGluGlyLysLeuAlaGlnAlaProPheProSerLeuGlyGlu	20
	CTAGCCGATCTCAAAAGACTTTTCGACGCCATTATTGTTCTTACAATGCCGCATGAACAA	
21	LeuAlaAspLeuLysArgLeuPheAspAlaIleIleValLeuThrMetProHisGluGln	40
	CCGCTTAATGAGAAATATATCGAGATATTAGAGAGCCATGGATTCCAAGTCCTCCATGTC	
41	ProLeuAsnGluLysTyrIleGluIleLeuGluSerHisGlyPheGlnValLeuHisVal	60
	CCCACGCTCGACTTTCATCCTTTAGAACTCTTCGACCTTTTGAAAACAAGCATATTCATT	
61	ProThrLeuAspPheHisProLeuGluLeuPheAspLeuLeuLysThrSerIlePheIle	80
	GATGAAAACCTGGAGAGATCCCACAGAGTGCTTGTCCACTGCATGGGAGGCATAGGCCGG	
81	AspGluAsnLeuGluArgSerHisArgValLeuValHisCysMetGlyGlyIleGlyArg	100
	AGCGGGCTTGTAACTGCTGCGTACTTAATATTCAAAGGTTATGATATTTACGACGCGGTA	
101	SerGlyLeuValThrAlaAlaTyrLeuIlePheLysGlyTyrAspIleTyrAspAlaVal	120
	AAGCATGTGAGAACGGTAGTGCCTGGTGCTATTGAAAACAGAGGGCAAGCGTTAATGCTT	
121	LysHisValArgThrValValProGlyAlaIleGluAsnArgGlyGlnAlaLeuMetLeu	140
	GAGAACTACTATACCCTGGTCAAAAGTTTCAACAGAGAGTTGCTGAGAGACTACGGGAAG	160
141	GluAsnTyrTyrThrLeuValLysSerPheAsnArgGluLeuLeuArgAspTyrGlyLys	160
	AAAATTTTCACGCTCGGTGACCCGAAGGCGGTTCTCCACGCTTCTAAGACGACTCAGTTC	
161	LysIlePheThrLeuGlyAspProLysAlaValLeuHisAlaSerLysThrThrGlnPhe	180
	ACGATTGAACTCTTAAGCAACTTACACGTCAACGAGGCGTTTTCAATCAGTGCGATGGCT	
181	ThrIleGluLeuLeuSerAsnLeuHisValAsnGluAlaPheSerIleSerAlaMetAla	200
	CAATCACTGCTCCACTTTCACGACGTAAAAGTCCGCTCTAAACTGAAAGAAGTATTCGAA	
201	GlnSerLeuLeuHisPheHisAspValLysValArgSerLysLeuLysGluValPheGlu	-220
	AACATGGAATTCTCATCCGCCTCAGAGGAGGTTCTGTCATTTATTCACCTACTCGATTTC	240
221	AsnMetGluPheSerSerAlaSerGluGluValLeuSerPheIleHisLeuLeuAspPhe	240
	TATCAGGATGGCAGGGTTGTTTTAACCATTTACGATTATCTCCCCGATAGGGTGGATTTG	
241	TyrGlnAspGlyArgValValLeuThrIleTyrAspTyrLeuProAspArgValAspLeu	260
	ATTTTATTGTGTAAGTGGGGTTGTGATAAAATAGTTGAAGTCTCGTCTTCAGCGAAGAAA	200
261	IleLeuLeuCysLysTrpGlyCysAspLysIleValGluValSerSerSerAlaLysLys	280
	ACCGTTGAGAAGCTTGTAGGAAGAAAGGTTTCCCTATCCTGGGCTAATTACTTAGACTAT	100
281	ThrValGlubysLeuValGlyArgLysValSerbeuSerTrpAlaAsnTyrLeuAspTyr	300

GTTTAG

301 ValEnd 302



Thermococcus CL-2 Phosphatase (30A1A) Complete Gene Sequence

	ATGAGAATCCTCCTCACCAACGACGGCATCTATTCCAACGGTCTGCGCGCGGCGGTG	
1	MetArgIleLeuLeuThrAsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaVal	20
	AAGGCCTGAGCGAGCTCGGCGAGGTCTACGTCGCCCCGCTCTTCCAGAGGAGCGCG	
21	LysGlyLeuSerGluLeuGlyGluValTyrValValAlaProLeuPheGlnArgSerAla	40
	AGCGGTCGGGCGATGACCCTACACAGGCCGATAAGGGCAAAGAGGGTTGACGTTCCCGGC	
41	SerGlyArgAlaMetThrLeuHisArgProIleArgAlaLysArgValAspValProGly	60
	GCGAAGATAGCGTATGGCATAGACGGAACGCCGACCGACTGCGTGATTTTTGCCATCGCC	00
61	AlaLysIleAlaTyrGlyIleAspGlyThrProThrAspCysValIlePheAlaIleAla	80
	CGCTTCGGCGACTTTGATCTGGCGGTCAGCGGGATAAACCTAGGCGAGAACCTGAGCACG	100
81	ArgPheGlyAspPheAspLeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThr	100
	GAGATAACCGTCTCCGGAACGGCCTCGGCGGCGATAGAGGCTTCCACCCAC	120
101	GluIleThrValSerGlyThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIlePro	120
	AGTGTAGCTATAAGCCTCGAGGTCGAGTGGAAGAAGACCCTCGGCGAGGGGGAGGGTATT	140
121	SerValAlaIleSerLeuGluValGluTrpLysLysThrLeuGlyGluGlyGluGlyIle	140
	GACTTCTCGGTTTCAGCACACTTCCTGAGAAGGATAGCGACGGCTGTCCTTAAGAAGGGC	1.00
141	AspPheSerValSerAlaHisPheLeuArgArgIleAlaThrAlaValLeuLysLysGly	160
	CTGCCTGAAGGGGTGGACATGCTCAACGTGAACGTCCCTAGCGACGCCAGCGAGGGGACT	
161	LeuProGluGlyValAspMetLeuAsnValAsnValProSerAspAlaSerGluGlyThr	180
	GAGATCGCCATAACGCGCCTCGCGAGGAAGCGCTATTCTCCGACGATAGAGGAGAGGATA	
181	GluIleAlaIleThrArgLeuAlaArgLysArgTyrSerProThrIleGluGluArgIle	200
	GACCCCAAGGGCAACCCCTACTACTGGATCGTTGGCAGGCTCGTCCAGGAGTTCGAGCCG	
201	AspProLysGlyAsnProTyrTyrTrpIleValGlyArgLeuValGlnGluPheGluPro	220
	GGCACGGACGCCTACGCTCTGAAAGTCGAGAGAAAGGTCAGCGTCACGCCCATAAACATC	
221	GlyThrAspAlaTyrAlaLeuLysValGluArgLysValSerValThrProIleAsnIle	240
	GACATGACTGCGAGGGTTGACTTTGAGAACCTTCAAAGGCTTCTGAGCCTGTGA	
2 / 1	AspMetThralaArgValAspPheGluAspLeuGlpArgLeuLeuSerLeuEnd 258	

261 GluValAlaValEnd 265

FIGURE /3

Aquifex VF-5 Phosphatase (34A1A) Complete Gene Sequence

	ATGGAAAACTTAAAAAAGTACCTAGAAGTTGCAAAAATAGCCGCGCTCGCGGGTGGGCAG	
1	MetGluAsnLeuLysLysTyrLeuGluValAlaLysIleAlaAlaLeuAlaGlyGlyGln	20
	GTTCTGAAAGAAAACTTCGGAAAGGTAAAAAAGGAAAAACATAGAGGAAAAAAGGGGAAAAAG	
21	ValLeuLysGluAsnPheGlyLysValLysLysGluAsnIleGluGluLysGlyGluLys	40
	GACTTTGTAAGTTACGTGGATAAAACTTCAGAGGAAAGGATAAAGGAGGTGATACTCAAG	
41	AspPheValSerTyrValAspLysThrSerGluGluArgIleLysGluValIleLeuLys	60
	TTCTTTCCCGATCACGAGGTCGTAGGGGAAGAGATGGGTGCGGAGGGAAGCGGAAGCGAA	
61	PhePheProAspHisGluValValGlyGluGluMetGlyAlaGluGlySerGlySerGlu	80
	TACAGGTGGTTCATAGACCCCCTTGACGGCACAAAGAACTACATAAACGGTTTTCCCATC	
81	TyrArgTrpPheIleAspProLeuAspGlyThrLysAsnTyrIleAsnGlyPheProIle	100
	TTTGCCGTATCAGTGGGACTTGTTAAGGGAGAAGAGCCAATTGTGGGTGCGGTTTACCTT	
101	PheAlaValSerValGlyLeuValLysGlyGluGluProIleValGlyAlaValTyrLeu	120
	CCTTACTTTGACAAGCTTTACTGGGGTGCTAAAGGTCTCGGGGCTTACGTAAACGGAAAG	
121	ProTyrPheAspLysLeuTyrTrpGlyAlaLysGlyLeuGlyAlaTyrValAsnGlyLys	140
	AGGATAAAGGTAAAGGACAATGAGAGTTTAAAGCACGCCGGAGTGGTTTACGGATTTCCC	
141	ArgIleLysValLysAspAsnGluSerLeuLysHisAlaGlyValValTyrGlyPhePro	160
	TCTAGGAGCAGGAGGACATATCTATCTACTTGAACATATTCAAGGATGTCTTTTACGAA	
161	SerArgSerArgArgAspIleSerIleTyrLeuAsnIlePheLysAspValPheTyrGlu	180
	GTTGGCTCTATGAGGAGACCCGGGGCTGCTGCGGTTGACCTCTGCATGGTGGCGGAAGGG	
181	ValGlySerMetArgArgProGlyAlaAlaAlaValAspLeuCysMetValAlaGluGly	200
	ATATTTGACGGGATGATGGAGTTTGAAATGAAGCCGTGGGACATAACCGCAGGGCTTGTA	
201	IlePheAspGlyMetMetGluPheGluMetLysProTrpAspIleThrAlaGlyLeuVal	220
	ATACTGAAGGAAGCCGGGGGCGTTTACACACTTGTGGGAGAACCCTTCGGAGTTTCGGAC	
221	<pre>IleLeuLysGluAlaGlyGlyValTyrThrLeuValGlyGluProPheGlyValSerAsp</pre>	240
	ATAATTGCGGGCAACAAAGCCCTCCACGACTTTATACTTCAGGTAGCCAAAAAGTATATG	
241	IleIleAlaGlyAsnLysAlaLeuHisAspPheIleLeuGlnValAlaLysLysTyrMet	260
	GAAGTGGCGGTGTGA	